

SEQUENCE LISTING

<110> Elan Corporation
O'Mahony, Daniel J.

<120> RETRO-INVERSION PEPTIDES THAT TARGET GIT TRANSPORT RECEPTORS AND
RELATED METHODS

<130> 25,478-A USA

<140> US 09/443,986

<141> 1999-11-19

<160> 85

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX2 15 mer fragment-D form retroinversion

<400> 1

Arg Thr Arg Leu Arg Arg Asn His Ser Ser His Lys Ala Asn Thr
1 5 10 15

<210> 2

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> P31 16 mer fragment- D form retroinversion

<400> 2

Gly Pro His Arg Arg Gly Arg Pro Asn Ser Arg Ser Ser Lys Arg Thr
1 5 10 15

<210> 3

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> HAX42 14 mer fragment-D form retroinversion

<400> 3

Gly Thr Ser Asn Gly Asn Gly Cys Cys Asn Tyr Asp Gly Pro
1 5 10

<210> 4

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX2 15 mer fragment

<400> 4

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> P31 16 mer fragment

<400> 5

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro Gly
1 5 10 15

<210> 6
<211> 14
<212> PRT
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<220>
<223> HAX42 14 mer fragment

<400> 6

Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10

<210> 7
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> PAX2 full length

<400> 7

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15

Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30

Arg Thr Arg Ser Arg Pro Asn Gly
35 40

<210> 8
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> HAX42 full length, N-terminal Lysine is dansylated

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Dansylated L-Lysine

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<400> 8

Lys Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15

Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
20 25 30

Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
35 40 45

<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> ZElan 144; PAX2 15 mer fragment-D form retroinversion with
addi tional L-lysine in position 1

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Dansylated L-lysine

<400> 9

Lys Arg Thr Arg Leu Arg Arg Asn His Ser Ser His Lys Ala Asn Thr
1 5 10 15

<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> ZElan 145; P31 16 mer fragment- D form retroinversion with
additi onal L-lysine in position 1

<220>
<221> MOD_RES
<222> (1)..(1)
<223> dansylated L-lysine

<400> 10

Lys Gly Pro His Arg Arg Gly Arg Pro Asn Ser Arg Ser Ser Lys Arg
1 5 10 15

Thr

<210> 11
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ZElan 146; HAX42 14 mer fragment-D form retroinversion with
addit ional L-Lysine in position 1

<220>
<221> MOD_RES
<222> (1)..(1)
<223> dansylated L-Lysine

<400> 11

Lys Gly Thr Ser Asn Gly Asn Gly Cys Cys Asn Tyr Asp Gly Pro
1 5 10 15

<210> 12
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> ZElan 129; PAX2 15 mer fragment with additional L-Lysine in
posi tion 1

<220>
<221> MOD_RES
<222> (1)..(1)
<223> dansylated L-Lysine

<400> 12

Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

<210> 13
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> ZElan 031; P31 16 mer fragment with additional L-Lysine in
positi on 1

<220>
<221> MOD_RES
<222> (1)..(1)
<223> dansylated L-Lysine

<400> 13

Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
1 5 10 15

Gly

<210> 14

<211> 15
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<213> Artificial Sequence

<220>
<223> ZElan 091; HAX42 14 mer fragment with additional L-lysine in
posi
tion 1

<220>
<221> MOD_RES
<222> (1)..(1)
<223> dansylated L-lysine

<400> 14

Lys Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

<210> 15
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> PAX2 full length, N-terminal Lysine is dansylated

<220>
<221> MOD_RES
<222> (1)..(1)
<223> dansylated L-Lysine

<400> 15

Lys Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val
1 5 10 15

Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
20 25 30

Leu Arg Thr Arg Ser Arg Pro Asn Gly
35 40

<210> 16
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> S15 44 mer fragment L-form

<400> 16

Arg Ser Gly Ala Tyr Glu Ser Pro Asp Gly Arg Gly Gly Arg Ser Tyr
1 5 10 15

Val Gly Gly Gly Gly Gly Cys Gly Asn Ile Gly Arg Lys His Asn Leu
20 25 30

Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp
5

35

40

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 <213> Artificial Sequence

<220>
 <223> S21 44 mer fragment L-form

<400> 17

Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly
 1 5 10 15

Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr
 20 25 30

Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser
 35 40

<210> 18
 <211> 44
 <212> PRT
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<220>
 <223> S22 44 mer fragment L-form

<400> 18

Ser Ser Ser Ser Asp Trp Gly Gly Val Pro Gly Lys Val Val Arg Glu
 1 5 10 15

Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr
 20 25 30

Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala
 35 40

<210> 19
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sni10 44 mer fragment L-form

<400> 19

Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg
 1 5 10 15

Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly
 20 25 30

Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His
 35 40

<210> 20
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Sni28 39 mer fragment L-form

<400> 20

Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu
1 5 10 15

Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro
20 25 30

Gln Leu Pro Arg Gly Pro Asn
35

<210> 21
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Sni34 41 mer fragment L-form

<400> 21

Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe
1 5 10 15

Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala
20 25 30

Ser Leu Glu Pro Pro Ser Ser Asp Tyr
35 40

<210> 22
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Sni38 39 mer fragment L-form

<400> 22

Arg Gly Ala Ala Asp Gln Arg Arg Gly Trp Ser Glu Asn Leu Gly Leu
1 5 10 15

Pro Arg Val Gly Trp Asp Ala Ile Ala His Asn Ser Tyr Thr Phe Thr
20 25 30

Ser Arg Arg Pro Arg Pro Pro
35

<210> 23
<211> 44
<212> PRT

<213> Artificial Sequence

<220>

<223> Sni45 44 mer fragment L-form

<400> 23

Ser Gly Gly Glu Val Ser Ser Trp Gly Arg Val Asn Asp Leu Cys Ala
1 5 10 15

Arg Val Ser Trp Thr Gly Cys Gly Thr Ala Arg Ser Ala Arg Thr Asp
20 25 30

Asn Lys Gly Phe Leu Pro Lys His Ser Ser Leu Arg
35 40

<210> 24

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> SniAX2 44 mer fragment L-form

<400> 24

Ser Asp Ser Asp Gly Asp His Tyr Gly Leu Arg Gly Gly Val Arg Cys
1 5 10 15

Ser Leu Arg Asp Arg Gly Cys Gly Leu Ala Leu Ser Thr Val His Ala
20 25 30

Gly Pro Pro Ser Phe Tyr Pro Lys Leu Ser Ser Pro
35 40

<210> 25

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> SniAX4 39 mer fragment L-form

<400> 25

Arg Ser Leu Gly Asn Tyr Gly Val Thr Gly Thr Val Asp Val Thr Val
1 5 10 15

Leu Pro Met Pro Gly His Ala Asn His Leu Gly Val Ser Ser Ala Ser
20 25 30

Ser Ser Asp Pro Pro Arg Arg
35

<210> 26

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> SniAX6 38 mer fragment L-form

<400> 26

Arg Thr Thr Thr Ala Lys Gly Cys Leu Leu Gly Ser Phe Gly Val Leu
1 5 10 15

Ser Gly Cys Ser Phe Thr Pro Thr Ser Pro Pro Pro His Leu Gly Tyr
20 25 30

Pro Pro His Ser Val Asn
35

<210> 27

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> SniAX8 39 mer fragment L-form

<400> 27

Ser Pro Lys Leu Ser Ser Val Gly Val Met Thr Lys Val Thr Glu Leu
1 5 10 15

Pro Thr Glu Gly Pro Asn Ala Ile Ser Ile Pro Ile Ser Ala Thr Leu
20 25 30

Gly Pro Arg Asn Pro Leu Arg
35

<210> 28

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> DAB3 39 mer fragment L-form

<400> 28

Arg Trp Cys Gly Ala Glu Leu Cys Asn Ser Val Thr Lys Lys Phe Arg
1 5 10 15

Pro Gly Trp Arg Asp His Ala Asn Pro Ser Thr His His Arg Thr Pro
20 25 30

Pro Pro Ser Gln Ser Ser Pro
35

<210> 29

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> DAB7 44 mer fragment L-form

<400> 29

Arg Trp Cys Gly Ala Asp Asp Pro Cys Gly Ala Ser Arg Trp Arg Gly
1 5 10 15

Gly Asn Ser Leu Phe Gly Cys Gly Leu Arg Cys Ser Ala Ala Gln Ser
20 25 30

Thr Pro Ser Gly Arg Ile His Ser Thr Ser Thr Ser
35 40

<210> 30
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> DAB10 39 mer fragment L-form

<400> 30

Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly Trp
1 5 10 15

Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp Tyr
20 25 30

Asn Gln Leu Pro Ser Asp Arg
35

<210> 31
<211> 38
<212> PRT
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<220>
<223> DAB18 38 mer fragment L-form

<400> 31

Arg Ser Ser Ala Asn Asn Cys Glu Trp Lys Ser Asp Trp Met Arg Arg
1 5 10 15

Ala Cys Ile Ala Arg Tyr Ala Asn Ser Ser Gly Pro Ala Arg Ala Val
20 25 30

Asp Thr Lys Ala Ala Pro
35

<210> 32
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DAB24 44 mer fragment L-form

<400> 32

Ser Lys Trp Ser Trp Ser Ser Arg Trp Gly Ser Pro Gln Asp Lys Val
1 5 10 15
10

Glu Lys Thr Arg Ala Gly Cys Gly Gly Ser Pro Ser Ser Thr Asn Cys
20 25 30

His Pro Tyr Thr Phe Ala Pro Pro Pro Gln Ala Gly
35 40

<210> 33
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DAB30 44 mer fragment L-form

<400> 33

Ser Gly Phe Trp Glu Phe Ser Arg Gly Leu Trp Asp Gly Glu Asn Arg
1 5 10 15

Lys Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser Ala Gln Gly
20 25 30

Pro Cys Pro Val Thr Pro Ala Thr Ile Asp Lys His
35 40

<210> 34
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DAX15 44 mer fragment L-form

<400> 34

Ser Glu Ser Gly Arg Cys Arg Ser Val Ser Arg Trp Met Thr Thr Trp
1 5 10 15

Gln Thr Gln Lys Gly Gly Cys Gly Ser Asn Val Ser Arg Gly Ser Pro
20 25 30

Leu Asp Pro Ser His Gln Thr Gly His Ala Thr Thr
35 40

<210> 35
<211> 39
<212> PRT
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<220>
<223> DAX23 39 mer fragment L-form

<400> 35

Arg Glu Trp Arg Phe Ala Gly Pro Pro Leu Asp Leu Trp Ala Gly Pro
1 5 10 15

Ser Leu Pro Ser Phe Asn Ala Ser Ser His Pro Arg Ala Leu Arg Thr
11

20

25

30

Tyr Trp Ser Gln Arg Pro Arg
35

<210> 36
<211> 44
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<213> Artificial Sequence

<220>
<223> DAX24 44 mer fragment L-form

<400> 36

Arg Met Glu Asp Ile Lys Asn Ser Gly Trp Arg Asp Ser Cys Arg Trp
1 5 10 15

Gly Asp Leu Arg Pro Gly Cys Gly Ser Arg Gln Trp Tyr Pro Ser Asn
20 25 30

Met Arg Ser Ser Arg Asp Tyr Pro Ala Gly Gly His
35 40

<210> 37
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> DAX27 36 mer fragment L-form

<400> 37

Ser His Pro Trp Tyr Arg His Trp Asn His Gly Asp Phe Ser Gly Ser
1 5 10 15

Gly Gln Ser Arg His Thr Pro Pro Glu Ser Pro His Pro Gly Arg Pro
20 25 30

Asn Ala Thr Ile
35

<210> 38
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX8 44 mer fragment L-form

<400> 38

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser
1 5 10 15

Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala
20 25 30

Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu
35 40

<210> 39
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX11 44 mer fragment L-form

<400> 39

Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr
1 5 10 15

Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr
20 25 30

Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
35 40

<210> 40
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX26 44 mer fragment L-form

<400> 40

Ser Gly Arg Thr Thr Ser Glu Ile Ser Gly Leu Trp Gly Trp Gly Asp
1 5 10 15

Asp Arg Ser Gly Tyr Gly Trp Gly Asn Thr Leu Arg Pro Asn Tyr Ile
20 25 30

Pro Tyr Arg Gln Ala Thr Asn Arg His Arg Tyr Thr
35 40

<210> 41
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX33 39 mer fragment L-form

<400> 41

Arg Trp Asn Trp Thr Val Leu Pro Ala Thr Gly Gly His Tyr Trp Thr
1 5 10 15

Arg Ser Thr Asp Tyr His Ala Ile Asn Asn His Arg Pro Ser Ile Pro
20 25 30

His Gln His Pro Thr Pro Ile
35

<210> 42
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX36 44 mer fragment L-form

<400> 42

Ser Trp Ser Ser Trp Asn Trp Ser Ser Lys Thr Thr Arg Leu Gly Asp
1 5 10 15

Arg Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
20 25 30

Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Thr
35 40

<210> 43
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX39 37 mer fragment L-form

<400> 43

Ser Gly Ser Leu Asn Ala Trp Gln Pro Arg Ser Trp Val Gly Gly Ala
1 5 10 15

Phe Arg Ser His Ala Asn Asn Asn Leu Asn Pro Lys Pro Thr Met Val
20 25 30

Thr Arg His Pro Thr
35

<210> 44
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> DCX42 44 mer fragment L-form

<400> 44

Arg Tyr Ser Gly Leu Ser Pro Arg Asp Asn Gly Pro Ala Cys Ser Gln
1 5 10 15

Glu Ala Thr Leu Glu Gly Cys Gly Ala Gln Arg Leu Met Ser Thr Arg
20 25 30

Arg Lys Gly Arg Asn Ser Arg Pro Gly Trp Thr Leu
35 40

<210> 45
<211> 39

<212> PRT
<213> Artificial Sequence

<220>
<223> DCX45 39 mer fragment L-form

<400> 45

Ser Val Gly Asn Asp Lys Thr Ser Arg Pro Val Ser Phe Tyr Gly Arg
1 5 10 15
Val Ser Asp Leu Trp Asn Ala Ser Leu Met Pro Lys Arg Thr Pro Ser
20 25 30

Ser Lys Arg His Asp Asp Gly
35

<210> 46
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> PAX9 38 mer fragment L-form

<400> 46

Arg Trp Pro Ser Val Gly Tyr Lys Gly Asn Gly Ser Asp Thr Ile Asp
1 5 10 15
Val His Ser Asn Asp Ala Ser Thr Lys Arg Ser Leu Ile Tyr Asn His
20 25 30

Arg Arg Pro Leu Phe Pro
35

<210> 47
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> PAX14 39 mer fragment L-form

<400> 47

Arg Thr Phe Glu Asn Asp Gly Leu Gly Val Gly Arg Ser Ile Gln Lys
1 5 10 15
Lys Ser Asp Arg Trp Tyr Ala Ser His Asn Ile Arg Ser His Phe Ala
20 25 30

Ser Met Ser Pro Ala Gly Lys
35

<210> 48
<211> 44
<212> PRT
<213> Artificial Sequence

<220>

<223> PAX15 44 mer fragment L-form

<400> 48

Ser Tyr Cys Arg Val Lys Gly Gly Gly Glu Gly Gly His Thr Asp Ser
1 5 10 15

Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu
20 25 30

Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg
35 40

<210> 49

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX16 39 mer fragment L-form

<400> 49

Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys
1 5 10 15

Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu
20 25 30

Pro Ser Asp Gln Gly Pro Pro
35

<210> 50

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX17 44 mer fragment L-form

<400> 50

Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser
1 5 10 15

Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Thr Arg
20 25 30

Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg
35 40

<210> 51

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX18 39 mer fragment L-form

<400> 51

Ser Phe Leu Arg Phe Gln Ser Pro Arg Phe Glu Asp Tyr Ser Arg Thr
1 5 10 15

Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala
20 25 30

His Asn Asn Arg Ala Leu Ala
35

<210> 52

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX35 39 mer fragment L-form

<400> 52

Arg Ser Ile Thr Asp Gly Gly Leu Asn Glu Val Asp Leu Ser Ser Val
1 5 10 15

Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His
20 25 30

Arg Pro Thr Leu Lys Arg Pro
35

<210> 53

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX38 44 mer fragment L-form

<400> 53

Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly
1 5 10 15

Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro
20 25 30

Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr
35 40

<210> 54

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> PAX40 44 mer fragment L-form

<400> 54

Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala
17

Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr
20 25 30

His Ala Pro His Arg Pro
35

<210> 58
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> P31 39 mer fragment L-form

<400> 58

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15

Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
20 25 30

Pro Arg Gly Arg Arg His Pro
35

<210> 59
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> P90 44 mer fragment L-form

<400> 59

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly
1 5 10 15

Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys
20 25 30

His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
35 40

<210> 60
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> 5PAX3 39 mer fragment L-form

<400> 60

Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala
1 5 10 15

Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys
20 25 30

His Lys Pro Leu Arg Arg Pro
35

<210> 61
<211> 39
<212> PRT
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<220>
<223> 5PAX5 39 mer fragment L-form
<400> 61

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn
1 5 10 15

Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr
20 25 30

Pro Ser Asn Arg Gly His Lys
35

<210> 62
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> 5PAX7 39 mer fragment L-form
<400> 62

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp
1 5 10 15

Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg
20 25 30

Val Leu Lys Ala Pro Leu Pro
35

<210> 63
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> 5PAX12 44 mer fragment L-form
<400> 63

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp
1 5 10 15

Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn
20 25 30

His Ala His Pro Ser His Gly Ala Val Ala Lys Ile
35 40

<210> 64
<211> 39
<212> PRT
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<220>
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<400> 64

Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His
1 5 10 15

Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro
20 25 30

Ala Asn Ser Gly Asp Pro Asn
35

<210> 65
<211> 44
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<223> HAX35 44 mer fragment L-form

<400> 65

Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp
1 5 10 15

Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
20 25 30

Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys
35 40

<210> 66
<211> 44
<212> PRT
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<220>
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<400> 66

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
1 5 10 15

Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
20 25 30

Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
35 40

<210> 67

<211> 44
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 <213> Artificial Sequence

 <220>
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 <400> 67
 Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
 1 5 10 15
 Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
 20 25 30

Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 35 40

<210> 68
 <211> 44
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HCA3 44 mer fragment L-form

 <400> 68
 Arg His Ile Ser Glu Tyr Ser Phe Ala Asn Ser His Leu Met Gly Gly
 1 5 10 15
 Glu Ser Lys Arg Lys Gly Cys Gly Ile Asn Gly Ser Phe Ser Pro Thr
 20 25 30
 Cys Pro Arg Ser Pro Thr Pro Ala Phe Arg Arg Thr
 35 40

<210> 69
 <211> 38
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 <220>
 <223> H40 38 mer fragment L-form

 <400> 69
 Ser Arg Glu Ser Gly Met Trp Gly Ser Trp Trp Arg Gly His Arg Leu
 1 5 10 15
 Asn Ser Thr Gly Gly Asn Ala Asn Met Asn Ala Ser Leu Pro Pro Asp
 20 25 30
 Pro Pro Val Ser Thr Pro
 35

<210> 70
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
<223> PAX2 39 mer fragment L-form
<400> 70

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15

Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30

Arg Thr Arg Ser Arg Pro Asn
35

<210> 71
<211> 1827
<212> PRT
<213> Artificial Sequence

<220>
<223> hSI receptor
<400> 71

Met Ala Arg Lys Lys Phe Ser Gly Leu Glu Ile Ser Leu Ile Val Leu
1 5 10 15

Phe Val Ile Val Thr Ile Ile Ala Ile Ala Leu Ile Val Val Leu Ala
20 25 30

Thr Lys Thr Pro Ala Val Asp Glu Ile Ser Asp Ser Thr Ser Thr Pro
35 40 45

Ala Thr Thr Arg Val Thr Thr Asn Pro Ser Asp Ser Gly Lys Cys Pro
50 55 60

Asn Val Leu Asn Asp Pro Val Asn Val Arg Ile Asn Cys Ile Pro Glu
65 70 75 80

Gln Phe Pro Thr Glu Gly Ile Cys Ala Gln Arg Gly Cys Cys Trp Arg
85 90 95

Pro Trp Asn Asp Ser Leu Ile Pro Trp Cys Phe Phe Val Asp Asn His
100 105 110

Gly Tyr Asn Val Gln Asp Met Thr Thr Thr Ser Ile Gly Val Glu Ala
115 120 125

Lys Leu Asn Arg Ile Pro Ser Pro Thr Leu Phe Gly Asn Asp Ile Asn
130 135 140

Ser Val Leu Phe Thr Thr Gln Asn Gln Thr Pro Asn Arg Phe Arg Phe
145 150 155 160

Lys Ile Thr Asp Pro Asn Asn Arg Arg Tyr Glu Val Pro His Gln Tyr
23

	165		170		175										
Val	Lys	Glu	Phe	Thr	Gly	Pro	Thr	Val	Ser	Asp	Thr	Leu	Tyr	Asp	Val
			180					185					190		
Lys	Val	Ala	Gln	Asn	Pro	Phe	Ser	Ile	Gln	Val	Ile	Arg	Lys	Ser	Asn
		195					200					205			
Gly	Lys	Thr	Leu	Phe	Asp	Thr	Ser	Ile	Gly	Pro	Leu	Val	Tyr	Ser	Asp
	210					215					220				
Gln	Tyr	Leu	Gln	Ile	Ser	Ala	Arg	Leu	Pro	Ser	Asp	Tyr	Ile	Tyr	Gly
225					230					235					240
Ile	Gly	Glu	Gln	Val	His	Lys	Arg	Phe	Arg	His	Asp	Leu	Ser	Trp	Lys
				245					250					255	
Thr	Trp	Pro	Ile	Phe	Thr	Arg	Asp	Gln	Leu	Pro	Gly	Asp	Asn	Asn	Asn
			260					265					270		
Asn	Leu	Tyr	Gly	His	Gln	Thr	Phe	Phe	Met	Cys	Ile	Glu	Asp	Thr	Ser
		275					280					285			
Gly	Lys	Ser	Phe	Gly	Val	Phe	Leu	Met	Asn	Ser	Asn	Ala	Met	Glu	Ile
	290					295					300				
Phe	Ile	Gln	Pro	Thr	Pro	Ile	Val	Thr	Tyr	Arg	Val	Thr	Gly	Gly	Ile
305					310					315					320
Leu	Asp	Phe	Tyr	Ile	Leu	Leu	Gly	Asp	Thr	Pro	Glu	Gln	Val	Val	Gln
				325					330					335	
Gln	Tyr	Gln	Gln	Leu	Val	Gly	Leu	Pro	Ala	Met	Pro	Ala	Tyr	Trp	Asn
			340					345					350		
Leu	Gly	Phe	Gln	Leu	Ser	Arg	Trp	Asn	Tyr	Lys	Ser	Leu	Asp	Val	Val
		355					360					365			
Lys	Glu	Val	Val	Arg	Arg	Asn	Arg	Glu	Ala	Gly	Ile	Pro	Phe	Asp	Thr
	370					375					380				
Gln	Val	Thr	Asp	Ile	Asp	Tyr	Met	Glu	Asp	Lys	Lys	Asp	Phe	Thr	Tyr
385					390					395					400
Asp	Gln	Val	Ala	Phe	Asn	Gly	Leu	Pro	Gln	Phe	Val	Gln	Asp	Leu	His
				405					410					415	
Asp	His	Gly	Gln	Lys	Tyr	Val	Ile	Ile	Leu	Asp	Pro	Ala	Ile	Ser	Ile
			420					425					430		
Gly	Arg	Arg	Ala	Asn	Gly	Thr	Thr	Tyr	Ala	Thr	Tyr	Glu	Arg	Gly	Asn
		435					440					445			

Thr Gln His Val Trp Ile Asn Glu Ser Asp Gly Ser Thr Pro Ile Ile
 450 455 460
 Gly Glu Val Trp Pro Gly Leu Thr Val Tyr Pro Asp Phe Thr Asn Pro
 465 470 475 480
 Asn Cys Ile Asp Trp Trp Ala Asn Glu Cys Ser Ile Phe His Gln Glu
 485 490 495
 Val Gln Tyr Asp Gly Leu Trp Ile Asp Met Asn Glu Val Ser Ser Phe
 500 505 510
 Ile Gln Gly Ser Thr Lys Gly Cys Asn Val Asn Lys Leu Asn Tyr Pro
 515 520 525
 Pro Phe Thr Pro Asp Ile Leu Asp Lys Leu Met Tyr Ser Lys Thr Ile
 530 535 540
 Cys Met Asp Ala Val Gln Asn Trp Gly Lys Gln Tyr Asp Val His Ser
 545 550 555 560
 Leu Tyr Gly Tyr Ser Met Ala Ile Ala Thr Glu Gln Ala Val Gln Lys
 565 570 575
 Val Phe Pro Asn Lys Arg Ser Phe Ile Leu Thr Arg Ser Thr Phe Ala
 580 585 590
 Gly Ser Gly Arg His Ala Ala His Trp Leu Gly Asp Asn Thr Ala Ser
 595 600 605
 Trp Glu Gln Met Glu Trp Ser Ile Thr Gly Met Leu Glu Phe Ser Leu
 610 615 620
 Phe Gly Ile Pro Leu Val Gly Ala Asp Ile Cys Gly Phe Val Ala Glu
 625 630 635 640
 Thr Thr Glu Glu Leu Cys Arg Arg Trp Met Gln Leu Gly Ala Phe Tyr
 645 650 655
 Pro Phe Ser Arg Asn His Asn Ser Asp Gly Tyr Glu His Gln Asp Pro
 660 665 670
 Ala Phe Phe Gly Gln Asn Ser Leu Leu Val Lys Ser Ser Arg Gln Tyr
 675 680 685
 Leu Thr Ile Arg Tyr Thr Leu Leu Pro Phe Leu Tyr Thr Leu Phe Tyr
 690 695 700
 Lys Ala His Val Phe Gly Glu Thr Val Ala Arg Pro Val Leu His Glu
 705 710 715 720

Phe Tyr Glu Asp Thr Asn Ser Trp Ile Glu Asp Thr Glu Phe Leu Trp
725 730 735
Gly Pro Ala Leu Leu Ile Thr Pro Val Leu Lys Gln Gly Ala Asp Thr
740 745 750
Val Ser Ala Tyr Ile Pro Asp Ala Ile Trp Tyr Asp Tyr Glu Ser Gly
755 760 765
Ala Lys Arg Pro Trp Arg Lys Gln Arg Val Asp Met Tyr Leu Pro Ala
770 775 780
Asp Lys Ile Gly Leu His Leu Arg Gly Gly Tyr Ile Ile Pro Ile Gln
785 790 795 800
Glu Pro Asp Val Thr Thr Thr Ala Ser Arg Lys Asn Pro Leu Gly Leu
805 810 815
Ile Val Ala Leu Gly Glu Asn Asn Thr Ala Lys Gly Asp Phe Phe Trp
820 825 830
Asp Asp Gly Glu Thr Lys Asp Thr Ile Gln Asn Gly Asn Tyr Ile Leu
835 840 845
Tyr Thr Phe Ser Val Ser Asn Asn Thr Leu Asp Ile Val Cys Thr His
850 855 860
Ser Ser Tyr Gln Glu Gly Thr Thr Leu Ala Phe Gln Thr Val Lys Ile
865 870 875 880
Leu Gly Leu Thr Asp Ser Val Thr Glu Val Arg Val Ala Glu Asn Asn
885 890 895
Gln Pro Met Asn Ala His Ser Asn Phe Thr Tyr Asp Ala Ser Asn Gln
900 905 910
Val Leu Leu Ile Ala Asp Leu Lys Leu Asn Leu Gly Arg Asn Phe Ser
915 920 925
Val Gln Trp Asn Gln Ile Phe Ser Glu Asn Glu Arg Phe Asn Cys Tyr
930 935 940
Pro Asp Ala Asp Leu Ala Thr Glu Gln Lys Cys Thr Gln Arg Gly Cys
945 950 955 960
Val Trp Arg Thr Gly Ser Ser Leu Ser Lys Ala Pro Glu Cys Tyr Phe
965 970 975
Pro Arg Gln Asp Asn Ser Tyr Ser Val Asn Ser Ala Arg Tyr Ser Ser
980 985 990

Met Gly Ile Thr Ala Asp Leu Gln Leu Asn Thr Ala Asn Ala Arg Ile
995 1000 1005

Lys Leu Pro Ser Asp Pro Ile Ser Thr Leu Arg Val Glu Val Lys
1010 1015 1020

Tyr His Lys Asn Asp Met Leu Gln Phe Lys Ile Tyr Asp Pro Gln
1025 1030 1035

Lys Lys Arg Tyr Glu Val Pro Val Pro Leu Asn Ile Pro Thr Thr
1040 1045 1050

Pro Ile Ser Thr Tyr Glu Asp Arg Leu Tyr Asp Val Glu Ile Lys
1055 1060 1065

Glu Asn Pro Phe Gly Ile Gln Ile Arg Arg Arg Ser Ser Gly Arg
1070 1075 1080

Val Ile Trp Asp Ser Trp Leu Pro Gly Phe Ala Phe Asn Asp Gln
1085 1090 1095

Phe Ile Gln Ile Ser Thr Arg Leu Pro Ser Glu Tyr Ile Tyr Gly
1100 1105 1110

Phe Gly Glu Val Glu His Thr Ala Phe Lys Arg Asp Leu Asn Trp
1115 1120 1125

Asn Thr Trp Gly Met Phe Thr Arg Asp Gln Pro Pro Gly Tyr Lys
1130 1135 1140

Leu Asn Ser Tyr Gly Phe His Pro Tyr Tyr Met Ala Leu Glu Glu
1145 1150 1155

Glu Gly Asn Ala His Gly Val Phe Leu Leu Asn Ser Asn Ala Met
1160 1165 1170

Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr Tyr Arg Thr Val
1175 1180 1185

Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro Thr Pro Gln
1190 1195 1200

Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro Val Met
1205 1210 1215

Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly Tyr
1220 1225 1230

Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala
1235 1240 1245

Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met
27

1250	1255	1260
Glu Arg Gln Leu Asp Phe Thr 1265 1270	Ile Gly Glu Ala Phe 1275	Gln Asp Leu
Pro Gln Phe Val Asp Lys Ile 1280 1285	Arg Gly Glu Gly Met 1290	Arg Tyr Ile
Ile Ile Leu Asp Pro Ala Ile 1295 1300	Ser Gly Asn Glu Thr 1305	Lys Thr Tyr
Pro Ala Phe Glu Arg Gly Gln 1310 1315	Gln Asn Asp Val Phe 1320	Val Lys Trp
Pro Asn Thr Asn Asp Ile Cys 1325 1330	Trp Ala Lys Val Trp 1335	Pro Asp Leu
Pro Asn Ile Thr Ile Asp Lys 1340 1345	Thr Leu Thr Glu Asp 1350	Glu Ala Val
Asn Ala Ser Arg Ala His Val 1355 1360	Ala Phe Pro Asp Phe 1365	Phe Arg Thr
Ser Thr Ala Glu Trp Trp Ala 1370 1375	Arg Glu Ile Val Asp 1380	Phe Tyr Asn
Glu Lys Met Lys Phe Asp Gly 1385 1390	Leu Trp Ile Asp Met 1395	Asn Glu Pro
Ser Ser Phe Val Asn Gly Thr 1400 1405	Thr Thr Asn Gln Cys 1410	Arg Asn Asp
Glu Leu Asn Tyr Pro Pro Tyr 1415 1420	Phe Pro Glu Leu Thr 1425	Lys Arg Thr
Asp Gly Leu His Phe Arg Thr 1430 1435	Ile Cys Met Glu Ala 1440	Glu Gln Ile
Leu Ser Asp Gly Thr Ser Val 1445 1450	Leu His Tyr Asp Val 1455	His Asn Leu
Tyr Gly Trp Ser Gln Met Lys 1460 1465	Pro Thr His Asp Ala 1470	Leu Gln Lys
Thr Thr Gly Lys Arg Gly Ile 1475 1480	Val Ile Ser Arg Ser 1485	Thr Tyr Pro
Thr Ser Gly Arg Trp Gly Gly 1490 1495	His Trp Leu Gly Asp 1500	Asn Tyr Ala
Arg Trp Asp Asn Met Asp Lys 1505 1510	Ser Ile Ile Gly Met 1515	Met Glu Phe

Ser Leu Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe
 1520 1525 1530
 Phe Asn Asn Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu
 1535 1540 1545
 Gly Ala Phe Tyr Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr
 1550 1555 1560
 Arg Arg Gln Asp Pro Ala Ser Trp Asn Glu Thr Phe Ala Glu Met
 1565 1570 1575
 Ser Arg Asn Ile Leu Asn Ile Arg Tyr Thr Leu Leu Pro Tyr Phe
 1580 1585 1590
 Tyr Thr Gln Met His Glu Ile His Ala Asn Gly Gly Thr Val Ile
 1595 1600 1605
 Arg Pro Leu Leu His Glu Phe Phe Asp Glu Lys Pro Thr Trp Asp
 1610 1615 1620
 Ile Phe Lys Gln Phe Leu Trp Gly Pro Ala Phe Met Val Thr Pro
 1625 1630 1635
 Val Leu Glu Pro Tyr Val Gln Thr Val Asn Ala Tyr Val Pro Asn
 1640 1645 1650
 Ala Arg Trp Phe Asp Tyr His Thr Gly Lys Asp Ile Gly Val Arg
 1655 1660 1665
 Gly Gln Phe Gln Thr Phe Asn Ala Ser Tyr Asp Thr Ile Asn Leu
 1670 1675 1680
 His Val Arg Gly Gly His Ile Leu Pro Cys Gln Glu Pro Ala Gln
 1685 1690 1695
 Asn Thr Phe Tyr Ser Arg Gln Lys His Met Lys Leu Ile Val Ala
 1700 1705 1710
 Ala Asp Asp Asn Gln Met Ala Gln Gly Ser Leu Phe Trp Asp Asp
 1715 1720 1725
 Gly Glu Ser Ile Asp Thr Tyr Glu Arg Asp Leu Tyr Leu Ser Val
 1730 1735 1740
 Gln Phe Asn Leu Asn Gln Thr Thr Leu Thr Ser Thr Ile Leu Lys
 1745 1750 1755
 Arg Gly Tyr Ile Asn Lys Ser Glu Thr Arg Leu Gly Ser Leu His
 1760 1765 1770

Val Trp Gly Lys Gly Thr Thr Pro Val Asn Ala Val Thr Leu Thr
1775 1780 1785

Tyr Asn Gly Asn Lys Asn Ser Leu Pro Phe Asn Glu Asp Thr Thr
1790 1795 1800

Asn Met Ile Leu Arg Ile Asp Leu Thr Thr His Asn Val Thr Leu
1805 1810 1815

Glu Glu Pro Ile Glu Ile Asn Trp Ser
1820 1825

<210> 72
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> D2H receptor

<400> 72

Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys
1 5 10 15

Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu
20 25 30

Gln Thr Pro Asp Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr
35 40 45

Arg Gly Ile Leu Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro
50 55 60

Tyr Ala Gly Met Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala
65 70 75 80

Arg Tyr Arg Ile Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser
85 90 95

Val Leu Val Leu Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro
100 105 110

Lys Cys Leu Asp Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro
115 120 125

Arg Ser Phe Lys Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly
130 135 140

Ile Gln Asp Lys Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val
145 150 155 160

Trp Ile Thr Ser Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly
165 170 175
30

Val Glu Asp Phe Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp
180 185 190
Phe Glu Asn Leu Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile
195 200 205
Ile Asp Phe Ile Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln
210 215 220
Leu Ser Arg Thr Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His
225 230 235 240
Asp Cys Thr His Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu
245 250 255
Ser Val Tyr Gly Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln
260 265 270
Cys Tyr Phe His Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg
275 280 285
Asn Pro Asp Val Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu
290 295 300
Thr Lys Gly Val Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu
305 310 315 320
Glu Ala Lys His Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile
325 330 335
Pro Asp Thr Val Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr
340 345 350
Thr Gln Val Gly Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met
355 360 365
Asp Gln Tyr Ser Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu
370 375 380
Ala Tyr Ala Glu Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro
385 390 395 400
Phe Ile Gln Glu Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu
405 410 415
Asp Thr Val Ser Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met
420 425 430
Glu Asn Met Pro Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro
435 440 445

Asp Ser Ser Arg Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val
450 455 460

Met Asn Met Leu Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr
465 470 475 480

Gly Glu Glu Ile Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu
485 490 495

Ser Tyr Asp Ile Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp
500 505 510

Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro
515 520 525

Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln
530 535 540

Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala
545 550 555 560

Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp
565 570 575

Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile
580 585 590

Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His
595 600 605

Asn Met Ile Ser Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr
610 615 620

Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu
625 630 635 640

Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu
645 650 655

His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala
660 665 670

Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys
675 680 685

<210> 73
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> binding 11 mer fragment L-form

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> "Xaa"=Ser or Thr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> "Xaa"=Arg or Lys

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> "Xaa"=Lys or Arg

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> "Xaa"=Ser or Leu

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> "Xaa"=Arg, Ile, Val, or Ser

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa"=Ser, Tyr, Phe, or His

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> "Xaa"=Phe, His, or Arg

<400> 73

Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg
1 5 10

<210> 74
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 8 mer fragment L-form

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> "Xaa"=Ser, Ala, or Gly

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> "Xaa"=Val or Glu

<220>

<221> MISC_FEATURE
<222> (7)..(7)
<223> "Xaa"= Pro, Gly, or Ser

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa" = Trp or Tyr

<400> 74

Asp Xaa Asp Xaa Arg Arg Xaa Xaa
1 5

<210> 75
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 10 mer fragment L-form

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> "Xaa"=Ala or Phe

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa"=Arg or His

<400> 75

Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser
1 5 10

<210> 76
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 11 mer fragment L-form

<400> 76

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg
1 5 10

<210> 77
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 11 mer fragment L-form

<400> 77

Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg
1 5 10

<210> 78
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 10 mer fragment L-form
<400> 78

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg
1 5 10

<210> 79
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 11 mer fragment L-form
<400> 79

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
1 5 10

<210> 80
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 8 mer fragment L-form
<400> 80

Asp Ser Asp Val Arg Arg Pro Trp
1 5

<210> 81
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 8 mer fragment L-form
<400> 81

Ala Ala Asp Gln Arg Arg Gly Trp
1 5

<210> 82
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 8 mer fragment L-form
<400> 82

Asp Gly Arg Gly Gly Arg Ser Tyr

1

5

<210> 83
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 4 mer fragment L-form

<400> 83

Arg Val Arg Ser
1

FL conclude
<210> 84
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 12 mer fragment L-form

<400> 84

Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser
1 5 10

<210> 85
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> binding 11 mer fragment L-form

<400> 85

Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser
1 5 10